

61735  
**STIC-Biotech/ChemLib**

**From:** Epps, Janet  
**Sent:** Thursday, February 28, 2002 1:49 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Sequence search request

Please search the following:

09/863,777

SEQ ID NO: 4-10

Search all commercial nucleic acid databases with the exception of the est databases.

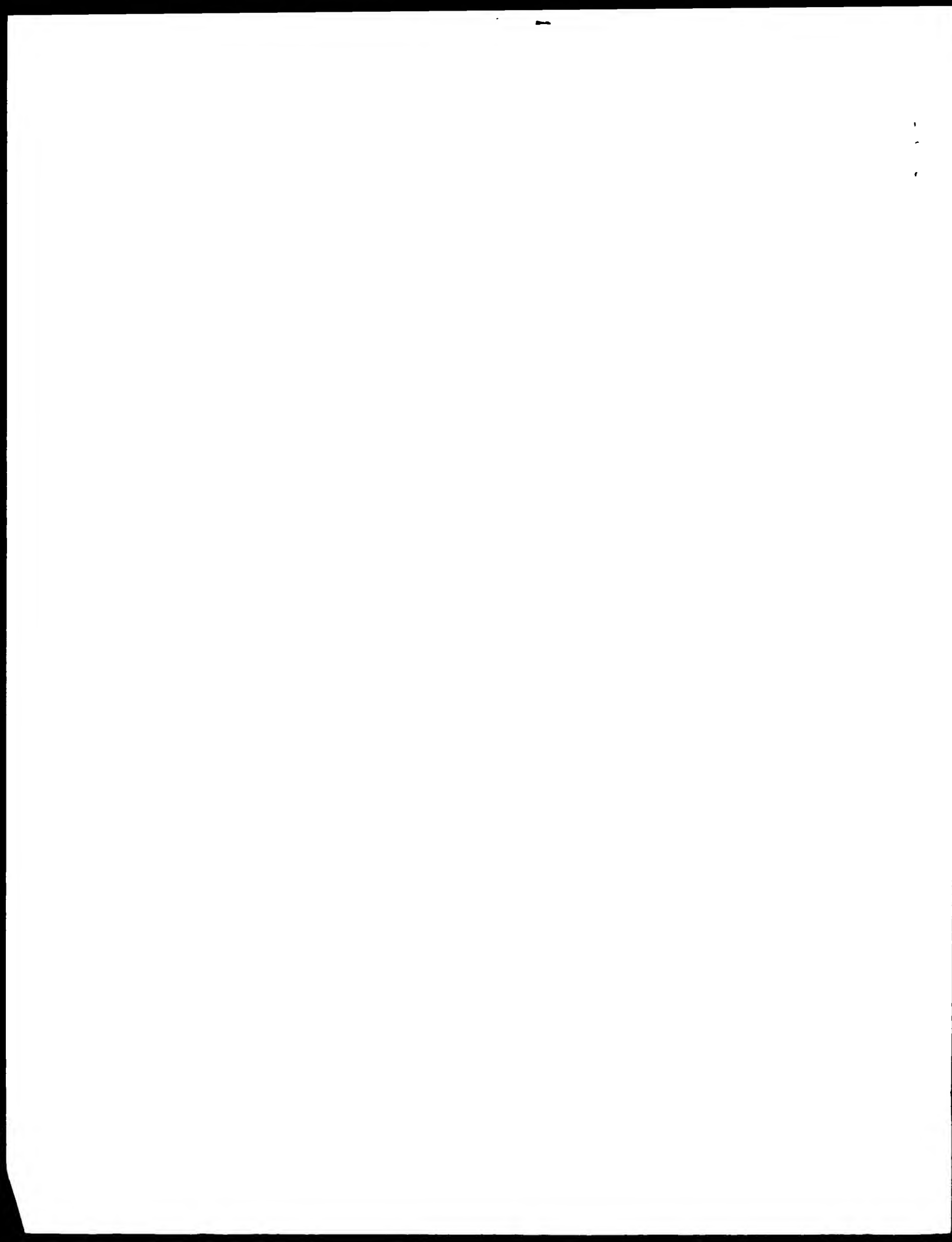
**Janet Epps**  
CM1 11E01  
United States Patent & Trademark Office  
**ART UNIT 1635 BIOTECH**  
703-308-8883  
janet.epps@uspto.gov

Point of Contact:  
Mona Smith  
Technical Information Specialist  
CM1 6A01  
Tel: 308-3278

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 3/1/02  
Date Completed: 3/5/02  
Searcher Prep/Review: 15  
Clerical: 4  
Online time: 15

TYPE OF SEARCH:  
NA Sequences: 7  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST(where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_









[illegible]



















[illegible]







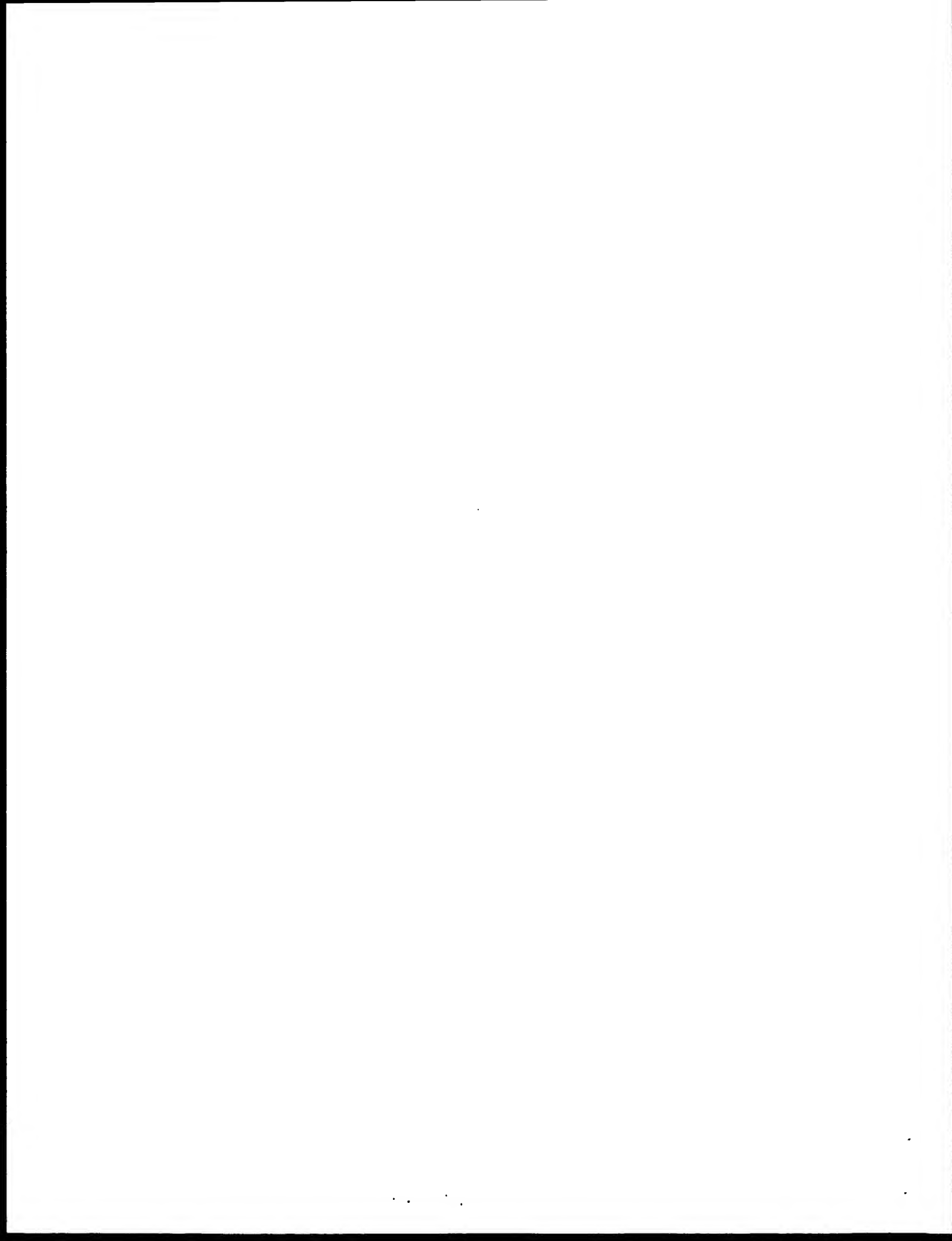












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FILED 3/5/02 15:07:57

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Copyright (c) 1999-2000 Veripoint Ltd.

Veripoint version 4.5

CH message needs to be sent to server SW model

Run on: March 5, 2002 12:52:13 - Search time 2514.8 seconds  
(Call of all messages)  
6.110 Millions of messages

Filter: us-09-863-777-5

Number of messages: 100000000

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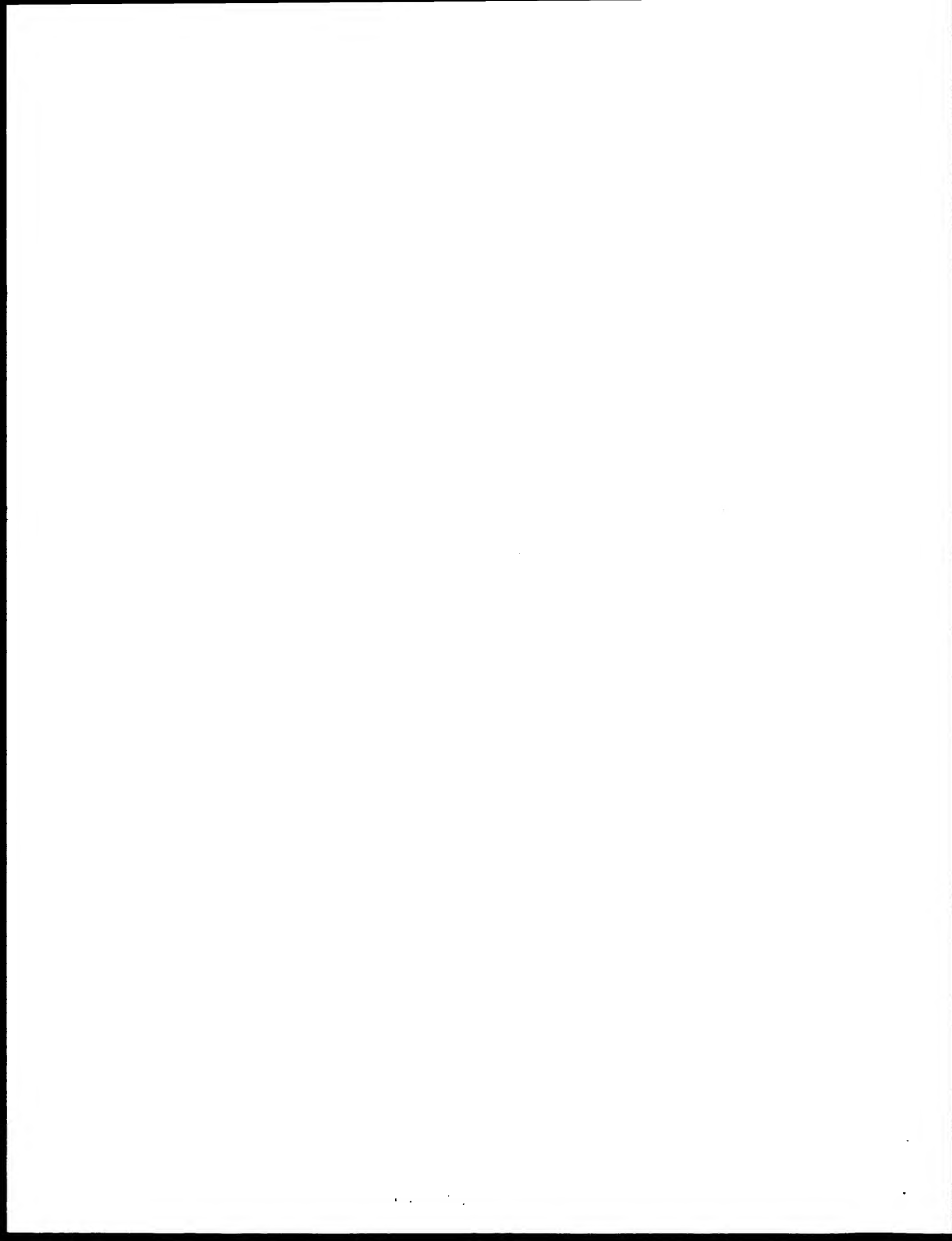












Copyright 1997-2000 Compuser Ltd.

Model: us-09-863-777-6

Search Time: 2087.42 seconds (without alignment)

Sequence: 1

Score: 14.214

Gap: 10.0

Score: 14.214

Score: 14.214

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BASE: 10000 4906 4 4 14 3 44741 4 4906 1  
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Matches: 17; Consistent: 0; Mismatches: 1; Indels: 0; Gaps: 0

25 1 acanmmscscdnnrta sw  
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 1111111111111111  
 1111111111111111

Search completed: Mar 5, 2002, 12:11:24  
 Tot. time: 500.00s



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us-09-863-777-6.rng

SUMMARY

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2	100.0	18	AAV1914	Antionin
3	100.0	18	AAV1915	Antionin
4	100.0	18	AAV1916	Antionin
5	100.0	18	AAV1917	Antionin
6	100.0	18	AAV1918	Antionin
7	100.0	18	AAV1919	Antionin
8	100.0	18	AAV1920	Antionin
9	100.0	18	AAV1921	Antionin
10	100.0	18	AAV1922	Antionin
11	100.0	18	AAV1923	Antionin
12	100.0	18	AAV1924	Antionin
13	100.0	18	AAV1925	Antionin
14	100.0	18	AAV1926	Antionin
15	100.0	18	AAV1927	Antionin
16	100.0	18	AAV1928	Antionin
17	100.0	18	AAV1929	Antionin
18	100.0	18	AAV1930	Antionin
19	100.0	18	AAV1931	Antionin
20	100.0	18	AAV1932	Antionin
21	100.0	18	AAV1933	Antionin
22	100.0	18	AAV1934	Antionin
23	100.0	18	AAV1935	Antionin
24	100.0	18	AAV1936	Antionin
25	100.0	18	AAV1937	Antionin
26	100.0	18	AAV1938	Antionin
27	100.0	18	AAV1939	Antionin
28	100.0	18	AAV1940	Antionin
29	100.0	18	AAV1941	Antionin
30	100.0	18	AAV1942	Antionin
31	100.0	18	AAV1943	Antionin
32	100.0	18	AAV1944	Antionin
33	100.0	18	AAV1945	Antionin
34	100.0	18	AAV1946	Antionin
35	100.0	18	AAV1947	Antionin
36	100.0	18	AAV1948	Antionin
37	100.0	18	AAV1949	Antionin
38	100.0	18	AAV1950	Antionin
39	100.0	18	AAV1951	Antionin
40	100.0	18	AAV1952	Antionin
41	100.0	18	AAV1953	Antionin
42	100.0	18	AAV1954	Antionin
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44	100.0	18	AAV1956	Antionin
45	100.0	18	AAV1957	Antionin
46	100.0	18	AAV1958	Antionin
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48	100.0	18	AAV1960	Antionin
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51	100.0	18	AAV1963	Antionin
52	100.0	18	AAV1964	Antionin
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94	100.0	18	AAV2006	Antionin
95	100.0	18	AAV2007	Antionin
96	100.0	18	AAV2008	Antionin
97	100.0	18	AAV2009	Antionin
98	100.0	18	AAV2010	Antionin
99	100.0	18	AAV2011	Antionin
100	100.0	18	AAV2012	Antionin





































\* consists of 28 entries, the true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary; gaps between the entries are represented as  
\* runs of N, but the exact sizes of the gaps are unknown;  
\* this record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 16261 16261; cont'd of 15268 bp in length  
16261 16261; gap of 100 bp  
16261 31621; cont'd of 1534 bp in length  
31621 31621; gap of 100 bp  
31621 52502; cont'd of 1998 bp in length  
52502 52502; gap of 100 bp  
52502 66551; cont'd of 1507 bp in length  
66551 66551; gap of 100 bp  
66551 92281; cont'd of 2271 bp in length  
92281 92281; gap of 100 bp  
92281 125791; cont'd of 3271 bp in length  
125791 125791; gap of 100 bp  
125791 159991; cont'd of 3271 bp in length  
159991 159991; gap of 100 bp  
159991 194821; cont'd of 3484 bp in length  
194821 194821; gap of 100 bp  
194821 224021; cont'd of 2829 bp in length  
224021 224021; gap of 100 bp  
224021 274551; cont'd of 1953 bp in length  
274551 274551; gap of 100 bp  
274551 301621; cont'd of 2627 bp in length  
301621 301621; gap of 100 bp  
301621 330981; cont'd of 3899 bp in length  
330981 330981; gap of 100 bp  
330981 381891; cont'd of 4001 bp in length  
381891 381891; gap of 100 bp  
381891 425581; cont'd of 4264 bp in length  
425581 425581; gap of 100 bp  
425581 472211; cont'd of 1521 bp in length  
472211 472211; gap of 100 bp  
472211 523311; cont'd of 4307 bp in length  
523311 523311; gap of 100 bp  
523311 575591; cont'd of 5328 bp in length  
575591 575591; gap of 100 bp  
575591 665511; cont'd of 8576 bp in length  
665511 665511; gap of 100 bp  
665511 730751; cont'd of 6640 bp in length  
730751 730751; gap of 100 bp  
730751 822711; cont'd of 9099 bp in length  
822711 822711; gap of 100 bp  
822711 899811; cont'd of 7512 bp in length  
899811 899811; gap of 100 bp  
899811 1022941; cont'd of 12411 bp in length  
1022941 1022941; gap of 100 bp  
1022941 1101351; cont'd of 8001 bp in length  
1101351 1101351; gap of 100 bp  
1101351 1248351; cont'd of 12660 bp in length  
1248351 1248351; gap of 100 bp  
1248351 1415921; cont'd of 19952 bp in length  
1415921 1415921; gap of 100 bp  
1415921 1642011; cont'd of 18409 bp in length  
1642011 1642011; gap of 100 bp  
1642011 1806211; cont'd of 26300 bp in length  
1806211 1806211; gap of 100 bp

FEATURES

1..16060  
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16261 16261; cont'd of 15268 bp in length  
16261 16261; gap of 100 bp  
16261 31621; cont'd of 1534 bp in length  
31621 31621; gap of 100 bp  
31621 52502; cont'd of 1998 bp in length  
52502 52502; gap of 100 bp  
52502 66551; cont'd of 1507 bp in length  
66551 66551; gap of 100 bp  
66551 92281; cont'd of 2271 bp in length  
92281 92281; gap of 100 bp  
92281 125791; cont'd of 3271 bp in length  
125791 125791; gap of 100 bp  
125791 159991; cont'd of 3271 bp in length  
159991 159991; gap of 100 bp  
159991 194821; cont'd of 3484 bp in length  
194821 194821; gap of 100 bp  
194821 224021; cont'd of 2829 bp in length  
224021 224021; gap of 100 bp  
224021 274551; cont'd of 1953 bp in length  
274551 274551; gap of 100 bp  
274551 301621; cont'd of 2627 bp in length  
301621 301621; gap of 100 bp  
301621 330981; cont'd of 3899 bp in length  
330981 330981; gap of 100 bp  
330981 381891; cont'd of 4001 bp in length  
381891 381891; gap of 100 bp  
381891 425581; cont'd of 4264 bp in length  
425581 425581; gap of 100 bp  
425581 472211; cont'd of 1521 bp in length  
472211 472211; gap of 100 bp  
472211 523311; cont'd of 4307 bp in length  
523311 523311; gap of 100 bp  
523311 575591; cont'd of 5328 bp in length  
575591 575591; gap of 100 bp  
575591 665511; cont'd of 8576 bp in length  
665511 665511; gap of 100 bp  
665511 730751; cont'd of 6640 bp in length  
730751 730751; gap of 100 bp  
730751 822711; cont'd of 9099 bp in length  
822711 822711; gap of 100 bp  
822711 899811; cont'd of 7512 bp in length  
899811 899811; gap of 100 bp  
899811 1022941; cont'd of 12411 bp in length  
1022941 1022941; gap of 100 bp  
1022941 1101351; cont'd of 8001 bp in length  
1101351 1101351; gap of 100 bp  
1101351 1248351; cont'd of 12660 bp in length  
1248351 1248351; gap of 100 bp  
1248351 1415921; cont'd of 19952 bp in length  
1415921 1415921; gap of 100 bp  
1415921 1642011; cont'd of 18409 bp in length  
1642011 1642011; gap of 100 bp  
1642011 1806211; cont'd of 26300 bp in length  
1806211 1806211; gap of 100 bp

2001. Match 94.44% (score 111.11) vs. (score 111.11)  
Best score 94.44% (score 111.11) vs. (score 111.11)  
Match 94.44% (score 111.11) vs. (score 111.11)

2. cont'd of 16261 bp  
3. cont'd of 16261 bp  
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11. cont'd of 16261 bp

12. cont'd of 16261 bp

13. cont'd of 16261 bp

14. cont'd of 16261 bp

## KEYWORDS

Genetic  
Genetics

## REFERENCES

Adams

## TITLE

Journal

## FEATURES

Source

## BASE

Genetic

## KEYWORD

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Search version 4.5

OR nucleotide nucleotide search using sw model

Run on: March 5, 2002, 22:11:57 : Search time 2037.42 Seconds  
(with hour adjustments)  
145,718 million cell updates/sec

Hit list: US 09 863-777-8

Footprint scores:

Sequence: 1 (max score) 19

Sequenced tables:

REPULIV NP  
Capo 1997, 1998, 1999

Searched: 147213 seqs, 924560755 residues

For a number of hits satisfying the chosen parameters: 2944280

Minimum 100 seq length: 1

Maximum seq length: 1000000

Foot print scoring: Minimum March 1997

Listed first 45 summaries

Total size:

GenBank:

- 1: ab\_101\*
- 2: ab\_101\*
- 3: ab\_101\*
- 4: ab\_101\*
- 5: ab\_101\*
- 6: ab\_101\*
- 7: ab\_101\*
- 8: ab\_101\*
- 9: ab\_101\*
- 10: ab\_101\*
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- 43: ab\_101\*
- 44: ab\_101\*
- 45: ab\_101\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Match Length	Hit	Seq
1	16.4	1000	11	11
2	16.4	1000	11	11
3	16.4	1000	11	11
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6	16.4	1000	11	11
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8	16.4	1000	11	11
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16	16.4	1000	11	11
17	16.4	1000	11	11
18	16.4	1000	11	11
19	16.4	1000	11	11
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43	16.4	1000	11	11
44	16.4	1000	11	11
45	16.4	1000	11	11









































XX 1. Suspensions of cells (24 hr) are prepared in 10% FBS medium.

XX 2. Cells are seeded into 96-well plates (100,000 cells per well) and grown for 24 hours.

XX 3. Cells are treated with various concentrations of the test compound for 24 hours.

XX 4. Cells are harvested and total RNA is extracted using RNeasy spin columns (Qiagen).

XX 5. Total RNA (100 ng) is reverse transcribed into cDNA using Superscript II reverse transcriptase (Life Technologies).

XX 6. cDNA is amplified by PCR using specific primers for the gene of interest.

XX 7. PCR products are electrophoresed on 2% agarose gels and stained with ethidium bromide.

XX 8. Gels are imaged under UV light and band intensity is quantified using a gel imaging system.

XX 9. Data are expressed as mean  $\pm$  SD of three independent experiments.

XX 10. Statistical significance is determined using Student's t-test.

XX 11. Results are presented as bar graphs.

XX 12. Error bars represent standard deviation.

XX 13. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001.

XX 14. All experiments were performed in triplicate.

XX 15. Data were analyzed using GraphPad Prism software.

XX 16. The results of the experiments are summarized in the following table.

XX 17. The table shows the effect of the test compound on the expression of the gene of interest.

XX 18. The data indicate that the test compound significantly increases the expression of the gene of interest.

XX 19. The effect is dose-dependent.

XX 20. The results are consistent with the hypothesis that the test compound acts as a transcriptional activator.

XX 21. Further studies are needed to elucidate the mechanism of action.

XX 22. The authors thank Dr. [Name] for his helpful discussions.

XX 23. This work was supported by [Funding Source].

XX 24. The authors have nothing to disclose.

XX 25. The authors have nothing to disclose.

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XX 99. The authors have nothing to disclose.

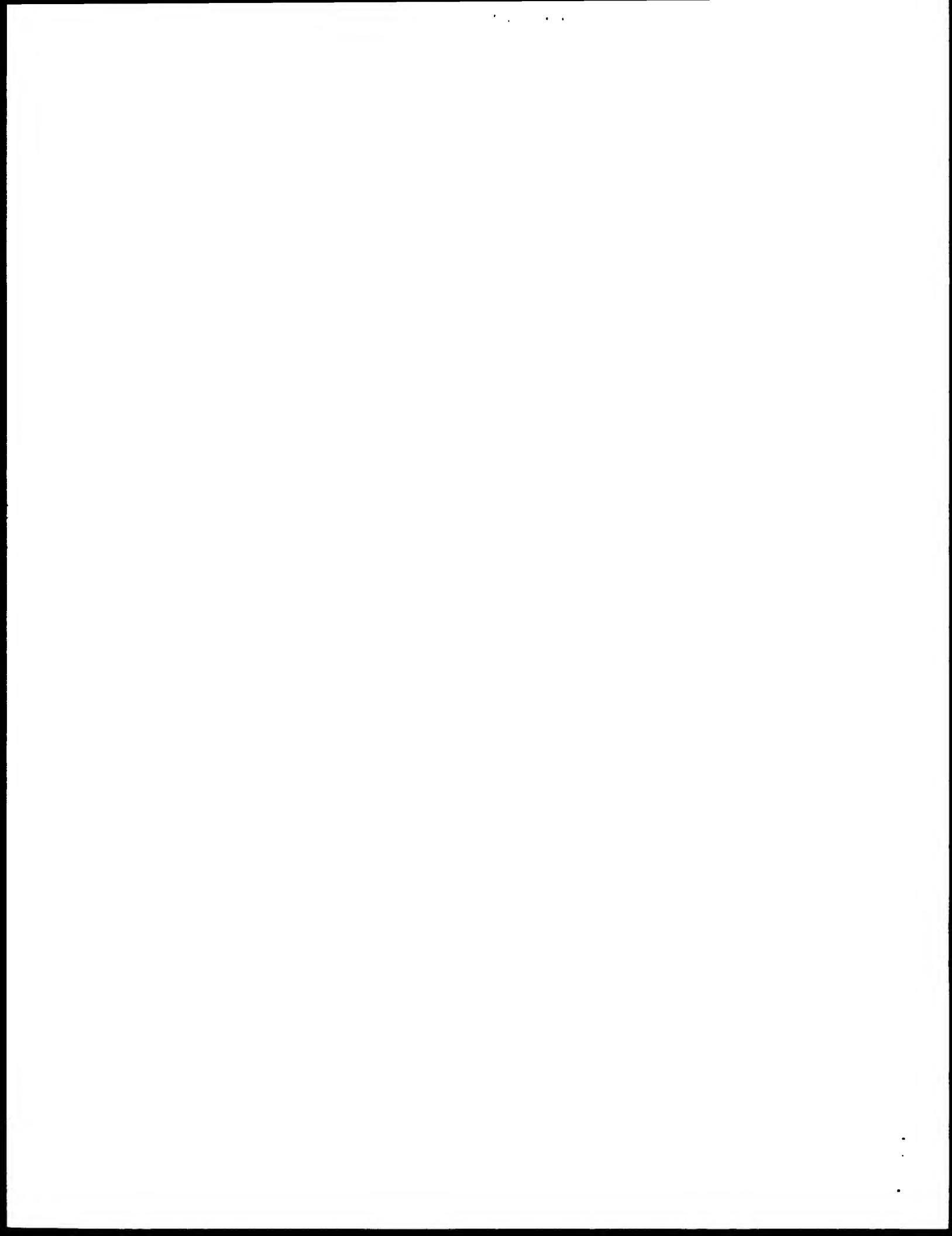
XX 100. The authors have nothing to disclose.











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Generation version 4.5

CR module: module search using ss model

Run on: March 5, 2002, 02:14:44 : Search time 2047.42 seconds  
(without alignments)

145,743 Million cells updated/s/seq

File: us-09-863-777-3

Per base scores:

Display: 1 average per site (seq 18)

Score table:

Identity No:

Gap: 100, 100, 100, 100

Search: 112,144 steps, 62,466,666 residues

100 number of hits satisfying chosen parameters: 2944280

Minimum 100 seq lengths:

Maximum 100 seq lengths: 1000000

Fast processing: Minimum 100 seq

Maximum 100 seq lengths: 1000000

Fast mode:

Genbank:

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2: ab\_1002\*

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12: ab\_1012\*

13: ab\_1013\*

14: ab\_1014\*

15: ab\_1015\*

16: ab\_1016\*

17: ab\_1017\*

18: ab\_1018\*

19: ab\_1019\*

20: ab\_1020\*

21: ab\_1021\*

22: ab\_1022\*

23: ab\_1023\*

24: ab\_1024\*

25: ab\_1025\*

26: ab\_1026\*

27: ab\_1027\*

28: ab\_1028\*

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33: ab\_1033\*

34: ab\_1034\*

35: ab\_1035\*

36: ab\_1036\*

37: ab\_1037\*

38: ab\_1038\*

39: ab\_1039\*

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43: ab\_1043\*

Summary:

Prod. No. in the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is defined by analyzing the total score distribution.



































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$\text{Mat}(C)$ ,  $x = x_0 \dots x_{n-1}$ : variable time ( $n$ )  
without adjustment ( $s_i$ )  
 $i=196$ . Minimum number  
of variables used:

[illegible][illegible][illegible][illegible]

Minimum	10	20	30	40	50	60	70	80	90	100
Minimum	10	20	30	40	50	60	70	80	90	100
Maximum	10	20	30	40	50	60	70	80	90	100

POST	POST-REVIEW	MINIMUM	MAXIMUM	Y
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1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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[illegible][illegible]

The figure consists of 15 small diagrams labeled (a) through (m), arranged vertically. Each diagram depicts a different stage of a parasite's life cycle, showing its morphology and how it interacts with its host or environment. The stages include eggs, larvae, and adult forms, some showing internal structures and others showing external features.

[illegible]

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For a complete list of the  $\mathcal{F}_i$  and  $\mathcal{F}_i^*$  in (1.1) see [1].

[illegible]

5.  $S \vdash \text{PMN} \vdash E: S$

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with shareholders, to undertake the necessary establishment of financial policy and to hold responsibility for the financial policy, to protect the interests of shareholders, to carry out the management with the goal of increasing the value of the shares.

the first two cases, the  $\mathcal{H}_2$  norm of the error signal is bounded by a constant that depends on the initial conditions of the system. In the third case, the  $\mathcal{H}_2$  norm of the error signal is bounded by a constant that depends on the initial conditions of the system and the magnitude of the disturbance.

1.  $\mathcal{A} = \mathcal{A}_1 \oplus \mathcal{A}_2$  and  $\mathcal{B} = \mathcal{B}_1 \oplus \mathcal{B}_2$  are  $\mathcal{A}$ - and  $\mathcal{B}$ -invariant subspaces of  $\mathcal{H}$  such that  $\mathcal{A}_1 \cap \mathcal{B}_1 = \{0\}$  and  $\mathcal{A}_2 \cap \mathcal{B}_2 = \{0\}$ .

Figure 1 illustrates the experimental setup. A participant is seated at a table, looking at a video screen. A camera is positioned above the screen to record movements. A light source is positioned to the left of the screen. A target is positioned on the screen. The participant's hand is positioned near the target. The diagram shows the spatial arrangement of the subject, camera, screen, light source, and target.

$$= \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

$\mathbb{A}^1$  is a  $\mathbb{G}_m$ -torsor over  $\mathbb{A}^1$  and  $\mathbb{A}^1$  is a  $\mathbb{G}_m$ -torsor over  $\mathbb{A}^1$ .

Human  $\alpha_1$ -antitrypsin, fully expressed, as opposed to the secreted protein, cDNA isolated from the liver of a patient with  $\alpha_1$ -antitrypsin deficiency (null allele) [19].

$$\begin{aligned} \mathbb{E}[\mathcal{L}_t] &= \mathbb{E}[\mathcal{L}_t^{\text{train}} + \mathcal{L}_t^{\text{test}}] \\ &= \mathbb{E}[\mathcal{L}_t^{\text{train}}] + \mathbb{E}[\mathcal{L}_t^{\text{test}}] \\ &= \mathbb{E}[\mathcal{L}_t^{\text{train}}] + \mathbb{E}[\mathcal{L}_t^{\text{test}}] \end{aligned}$$
[illegible][illegible][illegible]

Figure 1. The effect of the number of trials on the number of correct responses. The number of correct responses was plotted against the number of trials for each condition. The number of correct responses increased with the number of trials for all conditions. The number of correct responses was highest for the condition with the highest number of trials (10 trials) and lowest for the condition with the lowest number of trials (2 trials).

2. A second, nonparallel, line of  $25 \times 25$  points is placed in the middle and one of the two lines is rotated by  $45^\circ$  relative to the other. The two lines are then shifted apart by a distance of 100 units.

[illegible]

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum. Chl *a* is essential for the light-dependent reactions of photosynthesis, where it converts light energy into chemical energy.

2. *Chlorophyll b* (Chl *b*) is an accessory pigment found in green plants and algae. It is a yellow-green pigment that absorbs light energy in the blue and orange regions of the visible spectrum. Chl *b* transfers the absorbed energy to Chl *a* for use in photosynthesis.

3. *Carotenoids* are a group of pigments that include carotenes and xanthophylls. They are responsible for the yellow, orange, and red colors seen in autumn foliage. Carotenoids absorb light energy in the blue and green regions of the visible spectrum and transfer the energy to Chl *a*. They also play a role in protecting the photosynthetic apparatus from damage by reactive oxygen species.

4. *Anthocyanins* are water-soluble pigments that give plants their red, purple, and blue colors. They are not directly involved in photosynthesis but can protect the plant from damage by UV light and other environmental stressors.

5. *Flavonoids* are a large group of plant pigments that include flavones, flavanones, and flavonols. They are responsible for the yellow, white, and blue colors seen in many flowers. Flavonoids also play a role in plant defense and signaling.

[illegible]

Figure 1. The effect of the number of iterations on the accuracy of the proposed algorithm. The accuracy of the proposed algorithm increases with the number of iterations. The accuracy of the proposed algorithm is 0.9999 after 100 iterations.

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 207. *Tables*  
 208. *Figures*  
 209. *Supplementary Materials*  
 210. *Correspondence*  
 211. *Conflict of Interest*  
 212. *Acknowledgments*  
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 243. *Tables*  
 244. *Figures*  
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This is the nucleotide sequence of the human anti-oncogen gene. The invention relates to oligonucleotide compounds that inhibit the expression of anti-oncogen when administered to a mammal. Antisense phosphorothioate, lipid conjugates (see Example 17) that are complementary to critical regions of the anti-oncogen gene are claimed. The oligonucleotides of the invention are used in claimed methods to decrease production of dystonin, particularly to reduce the size of tumors associated with anti-oncogenes, to inhibit metastasis, establishment of tumor cells or growth of tumors and, when labeled, to detect anti-oncogen for diagnosis of conditions associated with abnormal anti-oncogenesis. They can also be used to treat a wide range of metastatic conditions that involve anti-oncogenes, e.g., metastatic nodular degeneration, diabetic retinopathy, bacterial or fungal ulcers, rheumatoid arthritis, heart disease, blood disease, hematoma and many others listed.

Significance: 4668 BP; 124° A; 109° P; 988 G; 1348 T; 0 other;

Quality Match	100.00	Score: 10	DB: 19	Length: 4668
Best Local Similarity	100.00	Prod. No. 17		
Matched	100.00	Cl. Matches	6	Index: 3
				Gar: 0

[illegible][illegible]

100

1715

$\text{NN} = \text{NN} + \text{NN}$

1.  $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$

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# THE ZEPHYRUS

$$Z = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-\frac{1}{2}x^2} dx = 1$$
[illegible]

*(continued)*

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[illegible]

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration was adjusted to 10<sup>8</sup> cells/ml. The cells were then mixed with the plant tissue and the transformation efficiency was determined. The results are shown as the mean ± SD of three independent experiments. The transformation efficiency was significantly different from the control (p < 0.05) by the Student's *t*-test.

11

[illegible]

Figure 1: Schematic representation of the experimental design. The diagram shows a flow from 'Stimulus' to 'Response' and 'Reaction time'. The 'Stimulus' is a 2x2 grid of images. The 'Response' is a 2x2 grid of images. The 'Reaction time' is a 2x2 grid of images. The 'Stimulus' and 'Response' are labeled 'Stimulus' and 'Response' respectively. The 'Reaction time' is labeled 'Reaction time'.

1. *Chlorophyll a* (Chl *a*)  
 2. *Chlorophyll b* (Chl *b*)  
 3. *Chlorophyll c* (Chl *c*)  
 4. *Chlorophyll d* (Chl *d*)  
 5. *Chlorophyll e* (Chl *e*)  
 6. *Chlorophyll f* (Chl *f*)  
 7. *Chlorophyll g* (Chl *g*)  
 8. *Chlorophyll h* (Chl *h*)  
 9. *Chlorophyll i* (Chl *i*)  
 10. *Chlorophyll j* (Chl *j*)  
 11. *Chlorophyll k* (Chl *k*)  
 12. *Chlorophyll l* (Chl *l*)  
 13. *Chlorophyll m* (Chl *m*)  
 14. *Chlorophyll n* (Chl *n*)  
 15. *Chlorophyll o* (Chl *o*)  
 16. *Chlorophyll p* (Chl *p*)  
 17. *Chlorophyll q* (Chl *q*)  
 18. *Chlorophyll r* (Chl *r*)  
 19. *Chlorophyll s* (Chl *s*)  
 20. *Chlorophyll t* (Chl *t*)  
 21. *Chlorophyll u* (Chl *u*)  
 22. *Chlorophyll v* (Chl *v*)  
 23. *Chlorophyll w* (Chl *w*)  
 24. *Chlorophyll x* (Chl *x*)  
 25. *Chlorophyll y* (Chl *y*)  
 26. *Chlorophyll z* (Chl *z*)  
 27. *Chlorophyll aa* (Chl *aa*)  
 28. *Chlorophyll ab* (Chl *ab*)  
 29. *Chlorophyll ac* (Chl *ac*)  
 30. *Chlorophyll ad* (Chl *ad*)  
 31. *Chlorophyll ae* (Chl *ae*)  
 32. *Chlorophyll af* (Chl *af*)  
 33. *Chlorophyll ag* (Chl *ag*)  
 34. *Chlorophyll ah* (Chl *ah*)  
 35. *Chlorophyll ai* (Chl *ai*)  
 36. *Chlorophyll aj* (Chl *aj*)  
 37. *Chlorophyll ak* (Chl *ak*)  
 38. *Chlorophyll al* (Chl *al*)  
 39. *Chlorophyll am* (Chl *am*)  
 40. *Chlorophyll an* (Chl *an*)  
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1.  $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$






































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THE UNIVERSITY OF CHICAGO (11.1.7)

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# REFERENCE

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